



## SEQUENCE LISTING

<110> Odgren, Paul R.  
Marks, Sandy C.  
Choi, Yongwon

<120> TRANCE REGULATION OF CHONDROCYTE  
DIFFERENTIATION

<130> 07917-120001

<140> 09/933,915  
<141> 2001-08-20

<150> 60/226,197  
<151> 2000-08-18

<160> 19

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 2226  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (157) ... (1107)

<400> 1  
ctcgacccac gcgtccgcgc gcccccaggag ccaaagccgg gctccaagtc ggcccccac 60  
gtcgaggctc cgccgcagcc tccggatgtt gccgcagaca agaaggggag ggagcgggag 120  
aggaggaga gctccgaagc gagagggccg agcgcc atg cgc cgc gcc agc aga 174  
Met Arg Arg Ala Ser Arg  
1 5

gac tac acc aag tac ctg cgt ggc tcg gag gag atg ggc ggc ggc ccc 222  
Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu Met Gly Gly Pro  
10 15 20

gga gcc ccg cac gag ggc ccc ctg cac gcc ccg ccg cct gcg ccg 270  
Gly Ala Pro His Glu Gly Pro Leu His Ala Pro Pro Pro Pro Ala Pro  
25 30 35

cac cag ccc ccc gcc tcc cgc tcc atg ttc gtg gcc ctc ctg ggg 318  
His Gln Pro Pro Ala Ala Ser Arg Ser Met Phe Val Ala Leu Leu Gly  
40 45 50

ctg ggg ctg ggc cag gtt gtc tgc agc gtc gcc ctg ttc tat ttc 366  
Leu Gly Leu Gly Gln Val Val Cys Ser Val Ala Leu Phe Phe Tyr Phe  
55 60 65 70

aga gcg cag atg gat cct aat aga ata tca gaa gat ggc act cac tgc 414  
Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys  
75 80 85



1 MRRASRDYTKYLRGSEEMGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQVVCSVALFFYF  
71 RAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIKQAFQGAVQKELQHIVGSQHI  
141 RAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSHKVSISSWYHDRGWAKISNMTFSNGKLIVNQ  
211 DGFYLYYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHYSINVGGF  
281 FKLRSGEEISIEVSNPSLLPDQDATYFGAFKVRDID (SEQ ID NO:2)

**FIG. 2**

att tat aga att ttg aga ctc cat gaa aat gca gat ttt caa gac aca Ile Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr	462
90 95 100	
act ctg gag agtcaa gat acaaa tta ata cct gat tca tgt agg aga Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg	510
105 110 115	
att aaa cag gcc ttt caa gga gct gtg caa aag gaa tta caa cat atc Ile Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile	558
120 125 130	
gtt gga tca cag cac atc aga gca gag aaa gcg atg gtg gat ggc tca Val Gly Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser	606
135 140 145 150	
tgg tta gat ctg gcc aag agg agc aag ctt gaa gct cag cct ttt gct Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala	654
155 160 165	
cat ctc act att aat gcc acc gac atc cca tct ggt tcc cat aaa gtg His Leu Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val	702
170 175 180	
agt ctg tcc tct tgg tac cat gat cgg ggt tgg gcc aag atc tcc aac Ser Leu Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn	750
185 190 195	
atg act ttt agc aat gga aaa cta ata gtt aat cag gat ggc ttt tat Met Thr Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr	798
200 205 210	
tac ctg tat gcc aac att tgc ttt cga cat cat gaa act tca gga gac Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp	846
215 220 225 230	
cta gct aca gag tat ctt caa cta atg gtg tac gtc act aaa acc agc Leu Ala Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser	894
235 240 245	
atc aaa atc cca agt tct cat acc ctg atg aaa gga gga agc acc aag Ile Lys Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys	942
250 255 260	
tat tgg tca ggg aat tct gaa ttc cat ttt tat tcc ata aac gtt ggt Tyr Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly	990
265 270 275	
gga ttt ttt aag tta cgg tct gga gag gaa atc agc atc gag gtc tcc Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser	1038
280 285 290	
aac ccc tcc tta ctg gat ccg gat cag gat gca aca tac ttt ggg gct Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala	1086
295 300 305 310	

ttt aaa gtt cga gat ata gat tgagccccag tttttggagt gttatgtatt 1137  
Phe Lys Val Arg Asp Ile Asp  
315

tccctggatgt	ttggaaacat	tttttaaaac	aagccaagaa	agatgtata	aggtgtgtga	1197
gactactaag	aggcatggcc	ccaaacggta	acgactca	atccatgctc	ttgaccttgt	1257
agagaacacg	cgtatttaca	gccagtgg	gatgttaga	tcatgtgt	ttacacaatg	1317
gtttttaaat	tttgtaatga	attccatgaa	ttaaaccaga	ttggagca	tacgggttga	1377
ccttatgaga	aactgcatgt	gggctatgg	aggggttgt	ccctggtc	gtgccccttc	1437
gcagctgaag	tggagagggt	gtcatctagc	gcaattgaag	gatcatctga	aggggcaat	1497
tcttttgaat	tgttacatca	tgctgaaacc	tgcaaaaaat	acttttcta	atgaggagag	1557
aaaatatatg	tatTTTata	taatatctaa	agttatattt	cagatgtat	gtttcttgc	1617
caaagtattg	taaattatat	ttgtgtata	gtatTTgatt	caaaatattt	aaaaatgtct	1677
tgctgttgac	atatttaatg	ttttaatgt	acagacat	ttaactgg	cactttgtaa	1737
attccctggg	gaaaacttgc	agctaaggag	gggaaaaaaaa	tgttgttcc	taatatcaaa	1797
tgcagtatat	ttcttcgttc	tttttaagtt	aatagattt	ttcagacttg	tcaagcctgt	1857
gcaaaaaat	taaaatggat	gccttgaata	ataagcagga	tgttgccac	caggtgcctt	1917
tcaaatttag	aaactaattt	actttagaaa	gctgacattt	ccaaaaagga	tacataatgg	1977
gccactgaaa	tctgtcaaga	gtagttat	aattgttga	caggtgttt	tccacaagtg	2037
ccgcaaattt	tacctttttt	ttttttcaa	aatagaaaaag	ttatttagtgg	tttatcagca	2097
aaaaagtcca	atTTtaattt	agtaaatgtt	atcttataact	gtacaataaa	aacattgcct	2157
ttgaatgtta	atTTTTtgtt	acaaaaataa	atttatatga	aaacctgaaa	aaaaaaaacaa	2217
aaaaaaaaaa						2226

<210> 2  
<211> 317  
<212> PRT  
<213> *Homo sapiens*

<400> 2  
 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu  
   1               5               10               15  
 Glu Met Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala  
   20               25               30  
 Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met  
   35               40               45  
 Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val  
   50               55               60  
 Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser  
   65               70               75               80  
 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn  
   85               90               95  
 Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile  
   100              105              110  
 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln  
   115              120              125  
 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys  
   130              135              140  
 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu  
   145              150              155              160  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro  
   165              170              175  
 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly  
   180              185              190  
 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val  
   195              200              205  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His

210	215	220
His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val		
225	230	235
Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met		240
245	250	255
Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe		
260	265	270
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu		
275	280	285
Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp		
290	295	300
Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp		
305	310	315

&lt;210&gt; 3

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 3

Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg		
1	5	10
Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg		
20	25	30
Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr		
35	40	45
Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His		
50	55	60
Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys		
65	70	75
Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys		
85	90	95
Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln		
100	105	110
Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His		
115	120	125
Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu		
130	135	140
Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser		
145	150	155
Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro		
165	170	175
Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp		
180	185	190

&lt;210&gt; 4

&lt;211&gt; 181

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu		
1	5	10
Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu		
20	25	30
Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu		
35	40	45

Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr  
 50 55 60  
 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu  
 65 70 75 80  
 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala  
 85 90 95  
 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys  
 100 105 110  
 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp  
 115 120 125  
 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe  
 130 135 140  
 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro  
 145 150 155 160  
 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys  
 165 170 175  
 Val Arg Asp Ile Asp  
 180

<210> 5  
 <211> 178  
 <212> PRT  
 <213> Homo sapiens

<400> 5

Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala  
 1 5 10 15  
 Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn  
 20 25 30  
 Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp  
 35 40 45  
 Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn  
 50 55 60  
 Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn  
 65 70 75 80  
 Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr  
 85 90 95  
 Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser  
 100 105 110  
 Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn  
 115 120 125  
 Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu  
 130 135 140  
 Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu  
 145 150 155 160  
 Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp  
 165 170 175  
 Ile Asp

<210> 6  
 <211> 173  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu

1	5	10	15												
Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Thr	Asp	Ile	Pro
20							25							30	
Ser	Gly	Ser	His	Lys	Val	Ser	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly
35							40					45			
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Phe	Ser	Asn	Gly	Lys	Leu	Ile	Val
50						55					60				
Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His
65					70				75				80		
His	Glu	Thr	Ser	Gly	Asp	Leu	Ala	Thr	Glu	Tyr	Leu	Gln	Leu	Met	Val
					85				90				95		
Tyr	Val	Thr	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Thr	Leu	Met
					100				105				110		
Lys	Gly	Gly	Ser	Thr	Lys	Tyr	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe
					115			120				125			
Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ser	Gly	Glu	Glu
					130			135			140				
Ile	Ser	Ile	Glu	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp
145					150				155				160		
Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Arg	Asp	Ile	Asp			
					165				170						

<210> 7  
<211> 160  
<212> PRT  
<213> Homo sapiens

1	5	10	15												
Ser	Lys	Leu	Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Thr
20							25							30	
Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Phe	Ser	Asn	Gly	Lys
35							40					45			
Leu	Ile	Val	Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys
50							55					60			
Phe	Arg	His	His	Glu	Thr	Ser	Gly	Asp	Leu	Ala	Thr	Glu	Tyr	Leu	Gln
65							70					75			80
Leu	Met	Val	Tyr	Val	Thr	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His
							85					90			95
Thr	Leu	Met	Lys	Gly	Gly	Ser	Thr	Lys	Tyr	Trp	Ser	Gly	Asn	Ser	Glu
							100			105			110		
Phe	His	Phe	Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ser
							115			120			125		
Gly	Glu	Glu	Ile	Ser	Ile	Glu	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro
							130			135			140		
Asp	Gln	Asp	Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Arg	Asp	Ile	Asp
145							150				155			160	

<210> 8  
<211> 159  
<212> PRT  
<213> Homo sapiens

1	5	10	15												
Lys	Leu	Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Thr	Asp

Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp  
 20 25 30  
 Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu  
 35 40 45  
 Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe  
 50 55 60  
 Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu  
 65 70 75 80  
 Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr  
 85 90 95  
 Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe  
 100 105 110  
 His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly  
 115 120 125  
 Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp  
 130 135 140  
 Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp  
 145 150 155

&lt;210&gt; 9

&lt;211&gt; 1945

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (95)...(826)

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1945)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 9

ctcntgtgnt cngggcgcct ggcctattga aggttttaa tcttcagagt ttcgacttta 60  
 tcaacaacac tttagaagcca ccaaagaatt gcag atg gat cct aat aga ata tca 115  
 Met Asp Pro Asn Arg Ile Ser  
 1 5

gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa aat 163  
 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn  
 10 15 20

gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta ata 211  
 Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile  
 25 30 35

cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg caa 259  
 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln  
 40 45 50 55

aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag aaa 307  
 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys  
 60 65 70

gcg atg gtg gat ggc tca tgg tta gat ctg gcc aag agg agc aag ctt 355  
 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu  
 75 80 85

gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc cca Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro	403
90 95 100	
tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg ggt Ser Gly Ser His Lys Val Ser Leu Ser Trp Tyr His Asp Arg Gly	451
105 110 115	
tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata gtt Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val	499
120 125 130 135	
aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga cat Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His	547
140 145 150	
cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg gtg His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val	595
155 160 165	
tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg atg Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met	643
170 175 180	
aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat ttt Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe	691
185 190 195	
tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag gaa Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu	739
200 205 210 215	
atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag gat Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp	787
220 225 230	
gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat tgagccccag Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp	836
235 240	
tttttgagt gttatgtatt tcctggatgt ttggaaacat tttttaaaac aagccaagaa agatgtatat aggtgtgtga gactactaag aggcatggcc ccaacggtag acgactcagt	896
atccatgctc ttgaccttgt agagaacacg cgtatttaca gccagtggga gatgttagac	956
tcatgggtgt ttacacaatg gtttttaaat tttgtatga attccttagaa ttaaaccaga	1016
ttggagcaat tacgggtga ccttatgaga aactgcattgt gggctatggg aggggttgtt	1076
ccctggcat gtgccttc gcagctgaag tggagagggt gtcatctagc gcaattgaag	1136
gatcatctga agggcataat tcttttgaat tgttacatca tgctggaaacc tgcaaaaaat	1196
acttttcta atgaggagag aaaatataatg tattttata taatatctaa agttatattt	1256
cagatgtaat gttttcttg caaagtattt taaattataat ttgtgtataa gtatttgatt	1316
caaaatattt aaaaatgtct tgctgttgac atattaatg ttttaaatgt acagacatata	1376
ttaactggtg cacttgtaa attccctggg gaaaacttgc agctaaggag gggaaaaaaaa	1436
tgttgttcc taatataaaa tgcaagtataat ttcttcgttc ttttaatgtt aatagatttt	1496
ttcagacttg tcaagcctgt gcaaaaaat taaaatggat gccttgaata ataagcagga	1556
tgtggccac caggtgcctt tcaaatttag aaactaatttgc acttttagaaa gctgacatttgc	1616
ccaaaaagga tacataatgg gccactgaaa tctgtcaaga gtagttat aatttgtgaa	1676
caggtgtttt tccacaatgt ccgcattt tacctttttt ttttttcaa aatagaaaaag	1736
	1796

ttatttagtgg tttatcagca aaaaagtcca attttaattt agtaaatgtt atcttatact	1856
gtacaataaa aacattgcct ttgaatgtta attttttgtt aaaaaataa atttatatga	1916
aacctgaaa aaaaaaaca aaaaaaaaaa	1945

<210> 10  
<211> 244  
<212> PRT  
<213> Homo sapiens

<400> 10  
Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr Arg  
1 5 10 15  
Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu  
20 25 30  
Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln  
35 40 45  
Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Ser  
50 55 60  
Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu Asp  
65 70 75 80  
Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr  
85 90 95  
Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser  
100 105 110  
Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe  
115 120 125  
Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr  
130 135 140  
Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr  
145 150 155 160  
Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile  
165 170 175  
Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser  
180 185 190  
Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe  
195 200 205  
Lys Leu Arg Ser Gly Glu Ile Ser Ile Glu Val Ser Asn Pro Ser  
210 215 220  
Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val  
225 230 235 240  
Arg Asp Ile Asp

<210> 11  
<211> 3136  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (39)...(1886)

<400> 11  
ccgctgaggc cgccggcgccc gccagcctgt cccgcgcc atg gcc ccg cgc gcc cg  
Met Ala Pro Arg Ala Arg  
1 5  
56

cg <sup>g</sup> cg <sup>c</sup> cg <sup>c</sup> cg <sup>c</sup> ct <sup>g</sup> tt <sup>c</sup> gc <sup>g</sup> ct <sup>g</sup> ct <sup>g</sup> ct <sup>c</sup> tc <sup>t</sup> gc <sup>g</sup> ct <sup>g</sup> ct <sup>c</sup> gc <sup>c</sup>	104
Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Cys Ala Leu Leu Ala	
10 15 20	
cg <sup>g</sup> ct <sup>g</sup> ca <sup>g</sup> gt <sup>g</sup> g <sup>c</sup> t <sup>t</sup> g <sup>c</sup> at <sup>c</sup> g <sup>c</sup> t <sup>c</sup> c <sup>c</sup> t <sup>t</sup> g <sup>t</sup> a <sup>c</sup> a <sup>g</sup> t <sup>a</sup> g <sup>a</sup> g <sup>a</sup> a <sup>g</sup>	152
Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys	
25 30 35	
ca <sup>t</sup> ta <sup>t</sup> ga <sup>g</sup> ca <sup>t</sup> ct <sup>g</sup> gg <sup>a</sup> cg <sup>g</sup> t <sup>g</sup> t <sup>t</sup> a <sup>a</sup> a <sup>aa</sup> t <sup>t</sup> g <sup>a</sup> a <sup>a</sup> cc <sup>a</sup> gg <sup>a</sup> a <sup>g</sup>	200
His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys	
40 45 50	
ta <sup>c</sup> at <sup>g</sup> t <sup>c</sup> t <sup>c</sup> t <sup>t</sup> a <sup>aa</sup> t <sup>g</sup> c <sup>o</sup> a <sup>c</sup> t <sup>c</sup> a <sup>c</sup> t <sup>c</sup> g <sup>a</sup> c <sup>t</sup> a <sup>g</sup> t <sup>a</sup> t <sup>t</sup> ct <sup>g</sup> cc <sup>c</sup>	248
Tyr Met Ser Ser Lys Cys Thr Thr Ser Asp Ser Val Cys Leu Pro	
55 60 65 70	
t <sup>t</sup> g <sup>g</sup> c <sup>c</sup> g <sup>a</sup> t <sup>t</sup> g <sup>a</sup> t <sup>a</sup> c <sup>c</sup> tt <sup>g</sup> g <sup>a</sup> t <sup>t</sup> a <sup>a</sup> g <sup>a</sup> g <sup>a</sup> g <sup>a</sup> t <sup>a</sup> a <sup>aa</sup> t <sup>t</sup> g <sup>c</sup>	296
Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys Cys	
75 80 85	
tt <sup>g</sup> ct <sup>g</sup> ca <sup>t</sup> a <sup>aa</sup> g <sup>t</sup> t <sup>t</sup> g <sup>a</sup> t <sup>a</sup> c <sup>a</sup> g <sup>g</sup> cc <sup>c</sup> ct <sup>g</sup> gt <sup>g</sup> gg <sup>c</sup> gt <sup>g</sup> g <sup>t</sup> c <sup>c</sup>	344
Leu Leu His Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val Val	
90 95 100	
gc <sup>c</sup> gg <sup>c</sup> aa <sup>c</sup> ag <sup>c</sup> ac <sup>g</sup> acc ccc cg <sup>g</sup> cg <sup>c</sup> t <sup>g</sup> gc <sup>g</sup> t <sup>g</sup> ac <sup>c</sup> g <sup>c</sup> t <sup>t</sup> ggg tac	392
Ala Gly Asn Ser Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly Tyr	
105 110 115	
ca <sup>c</sup> t <sup>g</sup> gg <sup>g</sup> ca <sup>g</sup> gac t <sup>g</sup> g <sup>a</sup> g t <sup>g</sup> c <sup>o</sup> t <sup>g</sup> c <sup>g</sup> c <sup>g</sup> a <sup>a</sup> c <sup>c</sup> g <sup>a</sup> g <sup>a</sup> t <sup>g</sup> c <sup>g</sup>	440
His Trp Ser Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys Ala	
120 125 130	
cc <sup>g</sup> gg <sup>c</sup> ct <sup>g</sup> gg <sup>c</sup> gg <sup>c</sup> ca <sup>g</sup> cac cc <sup>g</sup> tt <sup>g</sup> ca <sup>g</sup> ct <sup>c</sup> a <sup>a</sup> c <sup>a</sup> g <sup>a</sup> ac <sup>a</sup> g <sup>a</sup> t <sup>t</sup> g <sup>c</sup>	488
Pro Gly Leu Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr Val	
135 140 145 150	
t <sup>g</sup> c <sup>t</sup> a <sup>aa</sup> c <sup>c</sup> t <sup>t</sup> g <sup>c</sup> a <sup>g</sup> t <sup>g</sup> c <sup>t</sup> t <sup>c</sup> t <sup>t</sup> g <sup>a</sup> t <sup>t</sup> g <sup>c</sup> t <sup>t</sup> c <sup>c</sup> a <sup>g</sup> c <sup>t</sup>	536
Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser Thr	
155 160 165	
ga <sup>c</sup> a <sup>aa</sup> t <sup>g</sup> c <sup>t</sup> a <sup>g</sup> a <sup>cc</sup> t <sup>gg</sup> a <sup>c</sup> a <sup>a</sup> t <sup>t</sup> g <sup>t</sup> a <sup>c</sup> t <sup>t</sup> c <sup>tt</sup> g <sup>g</sup> a <sup>a</sup> g <sup>a</sup> a <sup>g</sup> a <sup>g</sup> g <sup>t</sup>	584
Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg Val	
170 175 180	
ga <sup>a</sup> ca <sup>t</sup> ca <sup>t</sup> gg <sup>g</sup> a <sup>c</sup> a <sup>g</sup> a <sup>aa</sup> t <sup>c</sup> c <sup>t</sup> g <sup>a</sup> t <sup>t</sup> g <sup>c</sup> g <sup>c</sup> t <sup>t</sup> t <sup>c</sup> t <sup>t</sup> ct <sup>g</sup>	632
Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu	
185 190 195	
cc <sup>a</sup> g <sup>c</sup> t <sup>t</sup> a <sup>aa</sup> cc <sup>a</sup> cc <sup>a</sup> a <sup>a</sup> t <sup>t</sup> g <sup>a</sup> cc <sup>c</sup> ca <sup>t</sup> g <sup>t</sup> t <sup>t</sup> c <sup>cc</sup> g <sup>gt</sup> t <sup>ta</sup>	680
Pro Ala Arg Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly Leu	
200 205 210	
at <sup>a</sup> at <sup>t</sup> ct <sup>g</sup> ct <sup>t</sup> ct <sup>c</sup> tt <sup>c</sup> gc <sup>g</sup> t <sup>t</sup> ct <sup>t</sup> gt <sup>g</sup> gc <sup>c</sup> ct <sup>g</sup> gt <sup>g</sup> g <sup>c</sup> at <sup>c</sup> at <sup>c</sup>	728
Ile Ile Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile Ile	
215 220 225 230	
tt <sup>t</sup> gg <sup>c</sup> g <sup>t</sup> t <sup>g</sup> c <sup>t</sup> a <sup>g</sup> a <sup>aa</sup> a <sup>aa</sup> gg <sup>g</sup> a <sup>a</sup> g <sup>c</sup> a <sup>c</sup> a <sup>g</sup> g <sup>t</sup> a <sup>a</sup> t <sup>t</sup> g <sup>t</sup>	776

Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn Leu			
235	240	245	
tgg cac tgg atc aat gag gct tgt ggc cgc cta agt gga gat aag gag			824
Trp His Trp Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys Glu			
250	255	260	
tcc tca ggt gac agt tgt gtc agt aca cac acg gca aac ttt ggt cag			872
Ser Ser Gly Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly Gln			
265	270	275	
cag gga gca tgt gaa ggt gtc tta ctg ctg act ctg gag gag aag aca			920
Gln Gly Ala Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys Thr			
280	285	290	
ttt cca gaa gat atg tgc tac cca gat caa ggt ggt gtc tgt cag ggc			968
Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln Gly Val Cys Gln Gly			
295	300	305	310
acg tgt gta gga ggt ggt ccc tac gca caa ggc gaa gat gcc agg atg			1016
Thr Cys Val Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg Met			
315	320	325	
ctc tca ttg gtc agc aag acc gag ata gag gaa gac agc ttc aga cag			1064
Leu Ser Leu Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg Gln			
330	335	340	
atg ccc aca gaa gat gaa tac atg gac agg ccc tcc cag ccc aca gac			1112
Met Pro Thr Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr Asp			
345	350	355	
cag tta ctg ttc ctc act gag cct gga agc aaa tcc aca cct cct ttc			1160
Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro Phe			
360	365	370	
tct gaa ccc ctg gag gtg ggg gag aat gac agt tta agc cag tgc ttc			1208
Ser Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys Phe			
375	380	385	390
acg ggg aca cag agc aca gtg ggt tca gaa agc tgc aac tgc act gag			1256
Thr Gly Thr Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr Glu			
395	400	405	
ccc ctg tgc agg act gat tgg act ccc atg tcc tct gaa aac tac ttg			1304
Pro Leu Cys Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr Leu			
410	415	420	
caa aaa gag gtg gac agt ggc cat tgc ccg cac tgg gca gcc agc ccc			1352
Gln Lys Glu Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser Pro			
425	430	435	
agc ccc aac tgg gca gat gtc tgc aca ggc tgc cg aac cct cct ggg			1400
Ser Pro Asn Trp Ala Asp Val Cys Thr Gly Cys Arg Asn Pro Pro Gly			
440	445	450	
gag gac tgt gaa ccc ctc gtg ggt tcc cca aaa cgt gga ccc ttg ccc			1448
Glu Asp Cys Glu Pro Leu Val Gly Ser Pro Lys Arg Gly Pro Leu Pro			

455	460	465	470	
cag tgc gcc tat ggc atg ggc ctt ccc cct gaa gaa gaa gcc agc agg Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro Glu Glu Ala Ser Arg				1496
475	480		485	
acg gag gcc aga gac cag ccc gag gat ggg gct gat ggg agg ctc cca Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly Ala Asp Gly Arg Leu Pro	490	495	500	1544
agc tca gcg agg gca ggt gcc ggg tct gga agc tcc cct ggt ggc cag Ser Ser Ala Arg Ala Gly Ser Gly Ser Ser Pro Gly Gly Gln	505	510	515	1592
tcc cct gca tct gga aat gtg act gga aac agt aac tcc acg ttc atc Ser Pro Ala Ser Gly Asn Val Thr Gly Asn Ser Asn Ser Thr Phe Ile	520	525	530	1640
535				
540				
tcc agc ggg cag gtg atg aac ttc aag ggc gac atc atc gtg gtc tac Ser Ser Gly Gln Val Met Asn Phe Lys Gly Asp Ile Ile Val Val Tyr	545			1688
550				
gtc agc cag acc tcg cag gag ggc gcg gcg gct gcg gag ccc atg Val Ser Gln Thr Ser Gln Glu Gly Ala Ala Ala Ala Ala Glu Pro Met	555	560	565	1736
565				
570				
575				
580				
ggc cgc ccg gtg cag gag acc ctg gcg cgc cga gac tcc ttc gcg Gly Arg Pro Val Gln Glu Thr Leu Ala Arg Arg Asp Ser Phe Ala	585	590	595	1784
595				
595				
ggg aac ggc ccg cgc ttc ccg gac ccg tgc ggc ggc ccc gag ggg ctg Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys Gly Pro Glu Gly Leu	595			1832
600				
605				
610				
aag gct tgagcgcccc ccatggctgg gagcccgaag ctcggagcca gggctcgca Lys Ala				1880
615				
ggcggcacc gcaaggctctg cccccagcccc ggccacccag ggatcgatcg gtacagtgcga ggaagaccac ccggcattct ctgcccactt tgcctccag gaaatggct ttccaggaag				1996
tgaattgtat aggactgtcc ccatgcccac ggatgctcag cagccgcgc cactggggca				2056
gatgtctccc ctgccactcc tcaaactcgc agcagaatt tgtggacta tgacagctat				2116
tttatatgact atcctttctt gtgggggggg ggtctatgtt ttccccccat atttgtattc				2176
cttttcataa cttttcttga tatctttctt ccctttttt taatgtaaaag gttttctcaa				2236
aaattctcct aaaggtgagg gtctttttt cttttttttt ttctttttt				2296
ggcaacctgg ctctggcca ggcttagagtg cagtggcgc attatagccc ggtgcagcct				2356
ctaactcctg ggctcaagca atccaaatgtt tcccccacc tcaacccatcg gagtagctgg				2416
gatcacagct gcaggccacg cccagcttc tccccccgac tccccccccc cagagacacg				2476
gtcccaccat gttaccctgc ctggctctcaa actccccagc taaagcagtc ctccagcctc				2536
ggcctcccaa agtactggta ttacaggcgt gagccccac gctggcctgc ttacgtatt				2596
ttcttttgc cccctgctca cagtgttttta gagatggctt tccctggctg tggttattgt				2656
aaacactttt gggaaaggc taaacatgtt aggcctggag atagttgcata agttgtttagg				2716
aacatgttggt gggactttca tattctgaaa aatgttctat attctcattt ttctaaaaga				2776
				2836

aagaaaaaaag	gaaaccggat	ttatttctcc	tgaatcttt	taagtttg	tcgttcctt	2896
agcagaacta	agctcagtat	gtgacccttac	ccgctagg	gttaatttat	ccatgctggc	2956
agaggcactc	aggtaacttgg	taagcaaatt	tctaaaactc	caagttgctg	cagcttggca	3016
ttcttcttat	tctagagg	tgc	aatggagaa	aatgaacagg	acatgggct	3076
cctggaaaga	aagggcccgg	gaagttcaag	gaagaataaa	gttgaat	taaaaaaaaaa	3136

&lt;210&gt; 12

&lt;211&gt; 616

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 12

Met	Ala	Pro	Arg	Ala	Arg	Arg	Arg	Arg	Pro	Leu	Phe	Ala	Leu	Leu	Leu
1				5					10						15
Leu	Cys	Ala	Leu	Leu	Ala	Arg	Leu	Gln	Val	Ala	Leu	Gln	Ile	Ala	Pro
				20				25						30	
Pro	Cys	Thr	Ser	Glu	Lys	His	Tyr	Glu	His	Leu	Gly	Arg	Cys	Cys	Asn
				35			40				45				
Lys	Cys	Glu	Pro	Gly	Lys	Tyr	Met	Ser	Ser	Lys	Cys	Thr	Thr	Thr	Ser
				50			55			60					
Asp	Ser	Val	Cys	Leu	Pro	Cys	Gly	Pro	Asp	Glu	Tyr	Leu	Asp	Ser	Trp
				65			70			75				80	
Asn	Glu	Glu	Asp	Lys	Cys	Leu	Leu	His	Lys	Val	Cys	Asp	Thr	Gly	Lys
				85			90						95		
Ala	Leu	Val	Ala	Val	Val	Ala	Gly	Asn	Ser	Thr	Thr	Pro	Arg	Arg	Cys
				100			105						110		
Ala	Cys	Thr	Ala	Gly	Tyr	His	Trp	Ser	Gln	Asp	Cys	Glu	Cys	Cys	Arg
				115			120					125			
Arg	Asn	Thr	Glu	Cys	Ala	Pro	Gly	Leu	Gly	Ala	Gln	His	Pro	Leu	Gln
				130			135				140				
Leu	Asn	Lys	Asp	Thr	Val	Cys	Lys	Pro	Cys	Leu	Ala	Gly	Tyr	Phe	Ser
				145			150				155			160	
Asp	Ala	Phe	Ser	Ser	Thr	Asp	Lys	Cys	Arg	Pro	Trp	Thr	Asn	Cys	Thr
					165			170				175			
Phe	Leu	Gly	Lys	Arg	Val	Glu	His	His	Gly	Thr	Glu	Lys	Ser	Asp	Ala
				180			185				190				
Val	Cys	Ser	Ser	Ser	Leu	Pro	Ala	Arg	Lys	Pro	Pro	Asn	Glu	Pro	His
				195			200				205				
Val	Tyr	Leu	Pro	Gly	Leu	Ile	Ile	Leu	Leu	Leu	Phe	Ala	Ser	Val	Ala
				210			215				220				
Leu	Val	Ala	Ala	Ile	Ile	Phe	Gly	Val	Cys	Tyr	Arg	Lys	Lys	Gly	Lys
				225			230			235			240		
Ala	Leu	Thr	Ala	Asn	Leu	Trp	His	Trp	Ile	Asn	Glu	Ala	Cys	Gly	Arg
					245			250				255			
Leu	Ser	Gly	Asp	Lys	Glu	Ser	Ser	Gly	Asp	Ser	Cys	Val	Ser	Thr	His
				260			265				270				
Thr	Ala	Asn	Phe	Gly	Gln	Gln	Gly	Ala	Cys	Glu	Gly	Val	Leu	Leu	Leu
				275			280				285				
Thr	Leu	Glu	Glu	Lys	Thr	Phe	Pro	Glu	Asp	Met	Cys	Tyr	Pro	Asp	Gln
				290			295				300				
Gly	Gly	Val	Cys	Gln	Gly	Thr	Cys	Val	Gly	Gly	Gly	Pro	Tyr	Ala	Gln
				305			310				315			320	
Gly	Glu	Asp	Ala	Arg	Met	Leu	Ser	Leu	Val	Ser	Lys	Thr	Glu	Ile	Glu
					325			330				335			
Glu	Asp	Ser	Phe	Arg	Gln	Met	Pro	Thr	Glu	Asp	Glu	Tyr	Met	Asp	Arg
					340			345				350			
Pro	Ser	Gln	Pro	Thr	Asp	Gln	Leu	Leu	Phe	Leu	Thr	Glu	Pro	Gly	Ser

355	360	365
Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp		
370	375	380
Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu		
385	390	395
Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met		
405	410	415
Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro		
420	425	430
His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly		
435	440	445
Cys Arg Asn Pro Pro Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro		
450	455	460
Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro		
465	470	475
Glu Glu Glu Ala Ser Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly		
485	490	495
Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly		
500	505	510
Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn		
515	520	525
Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly		
530	535	540
Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala		
545	550	555
Ala Ala Ala Glu Pro Met Gly Arg Pro Val Gln Glu Glu Thr Leu Ala		
565	570	575
Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys		
580	585	590
Gly Gly Pro Glu Gly Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val		
595	600	605
Gln Glu Gln Gly Gly Ala Lys Ala		
610	615	

&lt;210&gt; 13

&lt;211&gt; 2222

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (222)...(1787)

&lt;400&gt; 13

ccgcagctgg ggcttggcct gcgggcccc agcgaagggtg ggcgaaggctc ccactggatc	60
cagagtttgc cgtccaagca gcctcgatctc ggcgcgcagt gtctgtgtcc gtcctctacc	120
agcgccttgg ctgagcggag tcgtgcgggtt ggtgggggag ccctgccctc ctgggtcggc	180
ctccccgcgc actagaacga gcaagtata atcaagttac t atg agt ctg cta aac	236
Met Ser Leu Leu Asn	
1 5	

tgt gaa aac agc tgt gga tcc agc cag tct gaa agt gac tgc tgt gtg	284
Cys Glu Asn Ser Cys Gly Ser Ser Gln Ser Glu Ser Asp Cys Cys Val	
10 15 20	

gcc atg gcc agc tcc tgt agc gct gta aca aaa gat gat agt gtg ggt	332
Ala Met Ala Ser Ser Cys Ser Ala Val Thr Lys Asp Asp Ser Val Gly	

25	30	35	
gga act gcc agc acg ggg aac ctc tcc agc tca ttt atg gag gag atc Gly Thr Ala Ser Thr Gly Asn Leu Ser Ser Ser Phe Met Glu Glu Ile			380
40 45 50			
cag gga tat gat gta gag ttt gac cca ccc ctg gaa agc aag tat gaa Gln Gly Tyr Asp Val Glu Phe Asp Pro Pro Leu Glu Ser Lys Tyr Glu			428
55 60 65			
tgc ccc atc tgc ttg atg gca tta cga gaa gca gtg caa acg cca tgc Cys Pro Ile Cys Leu Met Ala Leu Arg Glu Ala Val Gln Thr Pro Cys			476
70 75 80 85			
ggc cat agg ttc tgc aaa gcc tgc atc ata aaa tca ata agg gat gca Gly His Arg Phe Cys Lys Ala Cys Ile Ile Lys Ser Ile Arg Asp Ala			524
90 95 100			
ggt cac aaa tgt cca gtt gac aat gaa ata ctg ctg gaa aat caa cta Gly His Lys Cys Pro Val Asp Asn Glu Ile Leu Glu Asn Gln Leu			572
105 110 115			
ttt cca gac aat ttt gca aaa cgt gag att ctt tct ctg atg gtg aaa Phe Pro Asp Asn Phe Ala Lys Arg Glu Ile Leu Ser Leu Met Val Lys			620
120 125 130			
tgt cca aat gaa ggt tgt ttg cac aag atg gaa ctg aga cat ctt gag Cys Pro Asn Glu Gly Cys Leu His Lys Met Glu Leu Arg His Leu Glu			668
135 140 145			
gat cat caa gca cat tgt gag ttt gct ctt atg gat tgt ccc caa tgc Asp His Gln Ala His Cys Glu Phe Ala Leu Met Asp Cys Pro Gln Cys			716
150 155 160 165			
cag cgt ccc ttc caa aaa ttc cat att aat att cac att ctg aag gat Gln Arg Pro Phe Gln Lys Phe His Ile Asn Ile His Ile Leu Lys Asp			764
170 175 180			
tgt cca agg aga cag gtt tct tgt gac aac tgt gct gca tca atg gca Cys Pro Arg Arg Gln Val Ser Cys Asp Asn Cys Ala Ala Ser Met Ala			812
185 190 195			
ttt gaa gat aaa gag atc cat gac cag aac tgt cct ttg gca aat gtc Phe Glu Asp Lys Glu Ile His Asp Gln Asn Cys Pro Leu Ala Asn Val			860
200 205 210			
atc tgt gaa tac tgc aat act ata ctc atc aga gaa cag atg cct aat Ile Cys Glu Tyr Cys Asn Thr Ile Leu Ile Arg Glu Gln Met Pro Asn			908
215 220 225			
cat tat gat cta gac tgc cct aca gcc cca att cca tgc aca ttc agt His Tyr Asp Leu Asp Cys Pro Thr Ala Pro Ile Pro Cys Thr Phe Ser			956
230 235 240 245			
act ttt ggt tgc cat gaa aag atg cag agg aat cac ttg gca cgc cac Thr Phe Gly Cys His Glu Lys Met Gln Arg Asn His Leu Ala Arg His			1004
250 255 260			

cta caa gag aac acc cag tca cac atg aga atg ttg gcc cag gct gtt Leu Gln Glu Asn Thr Gln Ser His Met Arg Met Leu Ala Gln Ala Val 265 270 275	1052
cat agt ttg agc gtt ata ccc gac tct ggg tat atc tca gag gtc cgg His Ser Leu Ser Val Ile Pro Asp Ser Gly Tyr Ile Ser Glu Val Arg 280 285 290	1100
aat ttc cag gaa act att cac cag tta gag ggt cgc ctt gta aga caa Asn Phe Gln Glu Thr Ile His Gln Leu Glu Gly Arg Leu Val Arg Gln 295 300 305	1148
gac cat caa atc cgg gag ctg act gct aaa atg gaa act cag agt atg Asp His Gln Ile Arg Glu Leu Thr Ala Lys Met Glu Thr Gln Ser Met 310 315 320 325	1196
tat gta agt gag ctc aaa cga acc att cga acc ctt gag gac aaa gtt Tyr Val Ser Glu Leu Lys Arg Thr Ile Arg Thr Leu Glu Asp Lys Val 330 335 340	1244
gct gaa atc gaa gca cag cag tgc aat gga att tat att tgg aag att Ala Glu Ile Glu Ala Gln Gln Cys Asn Gly Ile Tyr Ile Trp Lys Ile 345 350 355	1292
ggc aac ttt gga atg cat ttg aaa tgt caa gaa gag gag aaa cct gtt Gly Asn Phe Gly Met His Leu Lys Cys Gln Glu Glu Lys Pro Val 360 365 370	1340
gtg att cat agc cct gga ttc tac act ggc aaa ccc ggg tac aaa ctg Val Ile His Ser Pro Gly Phe Tyr Thr Gly Lys Pro Gly Tyr Lys Leu 375 380 385	1388
tgc atg cgc ttg cac ctt cag tta ccg act gct cag cgc tgt gca aac Cys Met Arg Leu His Leu Gln Leu Pro Thr Ala Gln Arg Cys Ala Asn 390 395 400 405	1436
tat ata tcc ctt ttt gtc cac aca atg caa gga gaa tat gac agc cac Tyr Ile Ser Leu Phe Val His Thr Met Gln Gly Glu Tyr Asp Ser His 410 415 420	1484
ctc cct tgg ccc ttc cag ggt aca ata cgc ctt aca att ctt gat cag Leu Pro Trp Pro Phe Gln Gly Thr Ile Arg Leu Thr Ile Leu Asp Gln 425 430 435	1532
tct gaa gca cct gta agg caa aac cac gaa gag ata atg gat gcc aaa Ser Glu Ala Pro Val Arg Gln Asn His Glu Glu Ile Met Asp Ala Lys 440 445 450	1580
cca gag ctg ctt gct ttc cag cga ccc aca atc cca cgg aac cca aaa Pro Glu Leu Leu Ala Phe Gln Arg Pro Thr Ile Pro Arg Asn Pro Lys 455 460 465	1628
ggt ttt ggc tat gta act ttt atg cat ctg gaa gcc cta aga caa aga Gly Phe Gly Tyr Val Thr Phe Met His Leu Glu Ala Leu Arg Gln Arg 470 475 480 485	1676

act ttc att aag gat gac aca tta tta gtg cgc tgt gag gtc tcc acc	1724	
Thr Phe Ile Lys Asp Asp Thr Leu Leu Val Arg Cys Glu Val Ser Thr		
490	495	500
cgc ttt gac atg ggt agc ctt cgg agg gag ggt ttt cag cca cga agt	1772	
Arg Phe Asp Met Gly Ser Leu Arg Arg Glu Gly Phe Gln Pro Arg Ser		
505	510	515
act gat gca ggg gta tagcttgccc tcacttgctc aaaaacaact acctggagaa	1827	
Thr Asp Ala Gly Val		
520		
aacagtgcct ttccttgccc tttctcaat aacatgcaaa caaacaagcc acggaaata	1887	
tgttatatct actagttagt gtgttagag aggtcaactt ctatttcttc tggttacaaa	1947	
tgtatcgagg cagtttttc ctggaatcc acacgttcca tgcttttca gaaatgttag	2007	
gcctgaagtg cctgtggcat gtgcagcag ctatttgcc agttagtata cctctttgtt	2067	
gtactttctt gggctttgc tctgggttat ttattgtca gaaagtccag actcaagagt	2127	
actaaacttt taataataat ggattttcct taaaacttca gtcttttgtt agtattat	2187	
gtaatatatt aaaagtaaaa atcactaccg ctttgc	2222	
<210> 14		
<211> 522		
<212> PRT		
<213> Homo sapiens		
 <400> 14		
Met Ser Leu Leu Asn Cys Glu Asn Ser Cys Gly Ser Ser Gln Ser Glu		
1 5 10 15		
Ser Asp Cys Cys Val Ala Met Ala Ser Ser Cys Ser Ala Val Thr Lys		
20 25 30		
Asp Asp Ser Val Gly Gly Thr Ala Ser Thr Gly Asn Leu Ser Ser Ser		
35 40 45		
Phe Met Glu Glu Ile Gln Gly Tyr Asp Val Glu Phe Asp Pro Pro Leu		
50 55 60		
Glu Ser Lys Tyr Glu Cys Pro Ile Cys Leu Met Ala Leu Arg Glu Ala		
65 70 75 80		
Val Gln Thr Pro Cys Gly His Arg Phe Cys Lys Ala Cys Ile Ile Lys		
85 90 95		
Ser Ile Arg Asp Ala Gly His Lys Cys Pro Val Asp Asn Glu Ile Leu		
100 105 110		
Leu Glu Asn Gln Leu Phe Pro Asp Asn Phe Ala Lys Arg Glu Ile Leu		
115 120 125		
Ser Leu Met Val Lys Cys Pro Asn Glu Gly Cys Leu His Lys Met Glu		
130 135 140		
Leu Arg His Leu Glu Asp His Gln Ala His Cys Glu Phe Ala Leu Met		
145 150 155 160		
Asp Cys Pro Gln Cys Gln Arg Pro Phe Gln Lys Phe His Ile Asn Ile		
165 170 175		
His Ile Leu Lys Asp Cys Pro Arg Arg Gln Val Ser Cys Asp Asn Cys		
180 185 190		
Ala Ala Ser Met Ala Phe Glu Asp Lys Glu Ile His Asp Gln Asn Cys		
195 200 205		
Pro Leu Ala Asn Val Ile Cys Glu Tyr Cys Asn Thr Ile Leu Ile Arg		
210 215 220		
Glu Gln Met Pro Asn His Tyr Asp Leu Asp Cys Pro Thr Ala Pro Ile		
225 230 235 240		
Pro Cys Thr Phe Ser Thr Phe Gly Cys His Glu Lys Met Gln Arg Asn		

245	250	255
His Leu Ala Arg His Leu Gln Glu Asn Thr Gln Ser His Met Arg Met		
260	265	270
Leu Ala Gln Ala Val His Ser Leu Ser Val Ile Pro Asp Ser Gly Tyr		
275	280	285
Ile Ser Glu Val Arg Asn Phe Gln Glu Thr Ile His Gln Leu Glu Gly		
290	295	300
Arg Leu Val Arg Gln Asp His Gln Ile Arg Glu Leu Thr Ala Lys Met		
305	310	315
Glu Thr Gln Ser Met Tyr Val Ser Glu Leu Lys Arg Thr Ile Arg Thr		
325	330	335
Leu Glu Asp Lys Val Ala Glu Ile Glu Ala Gln Gln Cys Asn Gly Ile		
340	345	350
Tyr Ile Trp Lys Ile Gly Asn Phe Gly Met His Leu Lys Cys Gln Glu		
355	360	365
Glu Glu Lys Pro Val Val Ile His Ser Pro Gly Phe Tyr Thr Gly Lys		
370	375	380
Pro Gly Tyr Lys Leu Cys Met Arg Leu His Leu Gln Leu Pro Thr Ala		
385	390	395
Gln Arg Cys Ala Asn Tyr Ile Ser Leu Phe Val His Thr Met Gln Gly		
405	410	415
Glu Tyr Asp Ser His Leu Pro Trp Pro Phe Gln Gly Thr Ile Arg Leu		
420	425	430
Thr Ile Leu Asp Gln Ser Glu Ala Pro Val Arg Gln Asn His Glu Glu		
435	440	445
Ile Met Asp Ala Lys Pro Glu Leu Leu Ala Phe Gln Arg Pro Thr Ile		
450	455	460
Pro Arg Asn Pro Lys Gly Phe Gly Tyr Val Thr Phe Met His Leu Glu		
465	470	475
480		
Ala Leu Arg Gln Arg Thr Phe Ile Lys Asp Asp Thr Leu Leu Val Arg		
485	490	495
Cys Glu Val Ser Thr Arg Phe Asp Met Gly Ser Leu Arg Arg Glu Gly		
500	505	510
Phe Gln Pro Arg Ser Thr Asp Ala Gly Val		
515	520	

<210> 15  
<211> 2237  
<212> DNA  
<213> Mus musculus

<400> 15

cccacgtccc	ggggagccac	tgccaggacc	tttgtgaacc	ggtcggggcg	ggggccgtgg	60
cggagtctgc	tcggcggtgg	gtggcccgag	aaggagaga	acgatcgccg	agcaggcgac	120
ccgaactccg	ggccgcgcgc	catgcgcgg	gccagccgag	actacggcaa	gtacctgcgc	180
agctcggaaag	agatggcag	cggccccggc	gtccccacacg	aagggtccgct	gcaccccgcg	240
ccttctgac	cggctccggc	gccgcccaccc	gccgcctccc	gctccatgtt	cctggccctc	300
ctggggctgg	gactgggcca	ggtggctgc	agcatcgctc	tgttcctgtt	ctttcgagcg	360
cagatggatc	ctaacagaat	atcagaagac	agcaactact	gctttatacg	aatcctgaga	420
ctccatgaaa	acgcaggtt	gcaggactcg	actctggaga	gtgaagacac	actacctgac	480
tcctgcagga	ggatgaaaca	agcccttcag	ggggccgtgc	agaaggaact	gcaacacatt	540
gtggggccac	agcgcttc	aggagctcca	gctatgatgg	aggctcatg	gttgatgtg	600
gcccagcgag	gcaagcctga	ggcccagcca	tttgcacacc	tcaccatcaa	tgctgccagc	660
atcccatcg	gttcccataa	agtcaactctg	tcctcttgg	accacgatcg	aggctggcc	720
aagatctcta	acatgacgtt	aagcaacgga	aaactaaggg	ttaaccaaga	tggcttctat	780
tacctgtacg	ccaacatttg	cttccggcat	catgaaaacat	cggaaagcgt	acctacagac	840
tatcttcagc	tgtatgggt	tgtcgtaaaa	accagcatca	aaatcccaag	ttctctataac	900

ctgatgaaag gagggagcac gaaaaactgg tcgggcaatt ctgaattcca ctttattcc	960
ataaatgttg ggggattttt caagctccga gctggtaag aaatttagat tcaggtgtcc	1020
aacccttccc tgctggatcc gcatcaagat gcgacgtact ttggggcttt caaagttcag	1080
gacatagact gagactcatt tcgtggaca tttagcatgga tgcctctagat gtttggaaac	1140
ttcttaaaaa atggatgatg tctatacatg tgtaagacta ctaagagaca tggcccacgg	1200
tgtatgaaac tcacaggccct ctctctttagag ccctgtacag gttgtgtata tgtaaagtcc	1260
ataggtgtatg ttagattcat ggtgattaca caacggtttt acaattttgt aatgatttcc	1320
tagaattgaa ccagattggg agaggtattc cgatgcttat gaaaaactta cacgtgagct	1380
atggaagggg gtcacagtct ctggctaaac ccctggacat gtgccactga gaaccttgaa	1440
attaagagga tgccatgtca ttgcataagaa atgatagtgt gaagggttaa gttctttga	1500
attgttacat tgcgctggga cctgcaaata agttctttt ttctaatgag gagaaaaata	1560
tatgtatTTT tatataatgt ctaaagttat atttcaggtg taatgtttc tgtgcaaagt	1620
tttggaaattt atatttgtc tatagtattt gattaaaaat attttaaaat gtctcaactgt	1680
tgacatattt aatgtttaa atgtacagat gtatttaact ggtgcacttt gtaattcccc	1740
tgaaggtaact cgtagctaag ggggcagaat actgtttctg gtgaccacat gtagttatt	1800
tctttattct tttaactta atagagtctt cagacttgc aaaactatgc aagcaaaata	1860
aataaataaaa aataaaatga ataccttga taataagttag gatgttggc accaggtgcc	1920
tttcaaattt agaagcta atgactttagg agctgacata gccaaaaagg aacataatag	1980
gctactgaaa tctgtcagga gtatttatgc aattattgaa caggtgtctt ttttacaag	2040
agctacaaat tggtaaattt ggttctttt ttttccata gaaaatgtac tatagtttat	2100
cagccaaaaaa acaatccact tttaatttta gtgaaagtta ttttattata ctgtacaata	2160
aaagcattgt ctctgaatgt taatttttg gtacaaaaaa taaatttgc cgaaaaaaa	2220
aaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa	2237

&lt;210&gt; 16

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 16

Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu			
1	5	10	15
Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro			
20	25	30	
Ala Pro Ser Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser			
35	40	45	
Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser			
50	55	60	
Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile			
65	70	75	80
Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu			
85	90	95	
Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro			
100	105	110	
Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys			
115	120	125	
Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala			
130	135	140	
Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu			
145	150	155	160
Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser			
165	170	175	
Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp			
180	185	190	
Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn			
195	200	205	
Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His			

210	215	220	
Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr			
225	230	235	240
Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys			
245	250	255	
Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr			
260	265	270	
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile			
275	280	285	
Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala			
290	295	300	
Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp			
305	310	315	

&lt;210&gt; 17

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

gagaggcccg agcgccatgc gccgcgccag cagagactac accaagtacc

50

&lt;210&gt; 18

&lt;211&gt; 60

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

ccaaagaatt gcagatggat cctaatagaa tatcagaaga tggcactcac tgcattata

60

&lt;210&gt; 19

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

ataatcaagt tactatgagt ctgctaaact gtgaaaacag ctgtggatcc a

51